

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:07:30 ; Search time 13.42 Seconds
(without alignments)
1009.824 Million cell updates/sec

Title: US-69-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONOSTDYTYEENEMNG.....VEEPPDSEGPTEPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105924 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	1	CKRB_HUMAN
2	1620	89.1	350	1	CKRB_BOVIN
3	659	36.2	378	1	CKR7_HUMAN
4	650	35.7	378	1	CKR7_MOUSE
5	639	35.1	359	1	CKR9_MOUSE
6	637	35.0	357	1	CKR9_HUMAN
7	605	33.3	367	1	CKR6_MOUSE
8	583	32.1	374	1	CKR6_HUMAN
9	581	31.9	342	1	CKR6_CERAE
10	571	31.4	343	1	CKR6_MACMU
11	569	30.8	342	1	CKR6_MACNE
12	560	30.8	342	1	CKR6_HUMAN
13	537.5	29.5	360	1	IL8B_HUMAN
14	534.5	29.4	360	1	IL8B_HUMAN
15	529.5	29.1	353	1	IL8B_HUMAN
16	525	28.9	353	1	IL8B_PANTR
17	524	28.8	354	1	CKR4_HUMAN
18	523	28.8	354	1	CKR4_HUMAN
19	522.5	28.7	353	1	IL8B_GORGO
20	522.5	28.7	353	1	CKR4_HUMAN
21	522.5	28.7	353	1	CKR4_MOUSE
22	521.5	28.6	353	1	IL8B_MOUSE
23	520.5	28.6	356	1	IL8B_CANFA
24	512	28.1	354	1	CKR3_MOUSE
25	511	28.1	354	1	IL8B_RABIT
26	511	28.1	354	1	IL8B_RABIT
27	504	27.7	360	1	CKR4_MOUSE
28	501.5	27.6	355	1	IL8B_MOUSE
29	501.5	27.6	355	1	IL8B_MOUSE
30	500.5	27.5	352	1	CKR3_CAVPO
31	499.5	27.5	352	1	CKR4_HUMAN
32	499.5	27.5	352	1	IL8B_BOVIN
33	498.5	27.4	352	1	CKR4_PAPAN

ALIGNMENTS

RESULT ID	CKRB_HUMAN	STANDARD	PRT	350 AA.
AC	09NPB9			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11)			
DE	(Chemokine receptor-like 1) (CCR1L) (CCX CKR)			
GN	CCR1L OR CCRP2 OR VSHK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20200450; PubMed=10734104;			
RA	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;			
RT	"CCR1L is a functional receptor for the monocyte chemoattractant protein family of chemokines."			
RL	J. Biol. Chem. 275:9550-9556(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2017178; PubMed=10706668;			
RA	Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,			
RA	Schall T.J.;			
RT	"Cutting edge: Identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK."			
RL	J. Immunol. 164:2851-2856(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20231748; PubMed=10767544;			
RA	Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;			
RT	"Cloning of CCR1L, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart."			
RL	Gene 246:229-238(2000).			
CC	- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4, SCYA19/MIP3B/ELC, SCYA21/SLC and SCYA23/TECK.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL TISSUES.			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL, AF193507; AAF61299.1; -			
DR	EMBL, AF233281; AAF44751.1; -			
DR	EMBL, AF110640; AAF59827.1; -			

DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_REC_P2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 43 63 POTENTIAL.
 FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 88 108 POTENTIAL.
 FT DOMAIN 109 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 114 134 POTENTIAL.
 FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 155 175 POTENTIAL.
 FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 202 222 POTENTIAL.
 FT DOMAIN 223 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 241 261 POTENTIAL.
 FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 290 310 POTENTIAL.
 FT DOMAIN 311 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 112 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.3e-104;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M A L E N O S T D Y Y E E N E N G T Y D Y S O Y E L I C I K E D V R E F A K F L P V F L T I V F V I G L A G N S 60
 DB 1 M A L E N O S T D Y Y E E N E N G T Y D Y S O Y E L I C I K E D V R E F A K F L P V F L T I V F V I G L A G N S 60
 QY 61 M V A I A Y A Y K K O R T K T D Y I I L N L A V A D L L F T L P F M A V N A V H G V L G K I M K I T S A L Y T 120
 DB 61 M V A I A Y A Y K K O R T K T D Y I I L N L A V A D L L F T L P F M A V N A V H G V L G K I M K I T S A L Y T 120
 QY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C M I I C F C W M A A I L I S P O L V F Y T V N D 180
 DB 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C M I I C F C W M A A I L I S P O L V F Y T V N D 180
 QY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C M I I C F C W M A A I L I S P O L V F Y T V N D 180
 DB 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C M I I C F C W M A A I L I S P O L V F Y T V N D 180
 QY 181 N A R C I P I P R Y L G T S M K A L I O M L E I C I G F V V P L I M G C Y F T A R T L M K M P N I K S R P L K 240
 DB 181 N A R C I P I P R Y L G T S M K A L I O M L E I C I G F V V P L I M G C Y F T A R T L M K M P N I K S R P L K 240
 QY 241 V L L E V V I F Y T O L P Y N I V K F C R A I D I Y S L I T S C N M S K R M D I A I O Y T E S I A L F H S C L N P 300
 DB 241 V L L E V V I F Y T O L P Y N I V K F C R A I D I Y S L I T S C N M S K R M D I A I O Y T E S I A L F H S C L N P 300
 QY 301 I L Y V F M G S F R N Y V A K V A K T I G S W R R O S V E E P F D S E G P T E P T S F S I 350
 DB 301 I L Y V F M G S F R N Y V A K V A K T I G S W R R O S V E E P F D S E G P T E P T S F S I 350

RESULT 2
 CRRB_BOVIN STANDARD; PRT; 350 AA.
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 11 (C-C-CCR-11) (CC-CCR-11) (CCR-11)
 DE (possible gustatory receptor type B) (ppr1 protein).
 GN CCR11.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE= Tongue;
 RX MEDLINE=93326166; PubMed=8392843;
 RA Matsuno I., Mori T., Aoki J., Sato T., Kurihara K.;
 RT "Identification of novel members of G-protein coupled receptor
 RL Superfamily expressed in bovine taste tissue";
 RT Biochem. Biophys. Res. Commun. 194:504-511(1993).
 CC - FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
 CC SCYA19/MIP3B/ELC, SCYA21/SIC and SCYA25/TECK (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
 CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
 CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
 CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: S63848; AAB27547.1; -
 DR PIR: JN0621; JN0621.
 DR GCRDB: GCR_0757; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_REC_P2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 42 66 1 (POTENTIAL).
 FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 80 99 2 (POTENTIAL).
 FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 114 135 3 (POTENTIAL).
 FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 154 175 4 (POTENTIAL).
 FT DOMAIN 176 199 5 (POTENTIAL).
 FT TRANSSEM 200 222 5 (POTENTIAL).
 FT DOMAIN 223 241 6 (POTENTIAL).
 FT TRANSSEM 242 265 6 (POTENTIAL).
 FT DOMAIN 266 283 7 (POTENTIAL).
 FT TRANSSEM 284 306 7 (POTENTIAL).
 FT DOMAIN 307 350 7 (POTENTIAL).
 FT CARBOHYD 6 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 89.1%; Score 1620; DB 1; Length 350;
 Best Local Similarity 86.0%; Pred. No. 1.8e-92;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 M A L E N O S T D Y Y E E N E N G T Y D Y S O Y E L I C I K E D V R E F A K F L P V F L T I V F V I G L A G N S 60
 DB 1 M A V E Y N O S T D Y Y E E N E M D T H D Y S O Y E I C I K E V R F A K F L P A F T I A I I G L A G N S 60
 QY 61 M V A I A Y A Y K K O R T K T D Y I I L N L A V A D L L F T L P F M A V N A V H G V L G K I M K I T S A L Y T 120
 DB 61 T V A I A Y A Y K K R R T K T D Y I I L N L A V A D L L F T L P F M A V N A V H G V L G K I M K V S A L Y T 120
 QY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C M I I C F C W M A A I L I S P O L V F Y T V N D 180
 DB 121 V N F V S G M O F L A C I S I D R Y A V A T K A P S O S G V G K P C W A A I L I S P O L V F Y T V N H 180
 QY 181 N A R C I P I P R Y L G T S M K A L I O M L E I C I G F V V P L I M G C Y F T A R T L M K M P N I K S R P L K 240
 DB 181 K A R C V P I P F Y H L G T S M K S I O L E I C I G F I I P L I M A V C Y F T A T L I K M P R I K S O P L K 240

DR	PROSITE: P50023/	G_PROTEIN_RECIP.F1.1; 1.
DR	PROSITE: P500262/	G_PROTEIN_RECIP.F1.2; 1.
KW	G-protein coupled receptor: Transmembrane; Glycoprotein; Signal.	
FT	CHAIN	1 24
FT	DOMAIN	25 378
FT	DOMAIN	25 59
FT	DOMAIN	60 86
FT	DOMAIN	87 95
FT	TRASMEM	96 116
FT	DOMAIN	117 130
FT	TRASMEM	131 152
FT	DOMAIN	153 170
FT	TRASMEM	171 191
FT	DOMAIN	192 219
FT	TRASMEM	220 247
FT	DOMAIN	248 263
FT	TRASMEM	264 289
FT	DOMAIN	290 313
FT	TRASMEM	314 331
FT	DOMAIN	332 378
FT	CAROHYD	36 36
FT	DISULF	129 210
FT	CONFLICT	182 183
FT	CONFLICT	337 337
SO	SEQUENCE	378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;

Query Match	Best Local Similarity	Score 659;	DB 1;	Length 378;
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps
QY 1	MALEQNSTDYDYEEENENNGTYDYSOYELEIKEDVEEFAKVPFLPYELTYVYGLAGNS	60		
DB 21	VCLQDEVTDDYIGDNT---TVDTLPESLCSKSDVNRKAFMLPMKSTICEFVGLGNG	77		
QY 61	MYVAIAYYKKQKFKRTDVIYILMAVDLLFTLPENAVNAHVGWVGLKIMCKITSALYT	120		
DB 78	LVLVLYIYFKRLKTMFTDTYLLNLAVADILFLFLTPMAVSAKSWGVNHPCKLIFAIYK	137		
QY 121	LNFGSMQFLACISIDRYVANTKPS-----QSGVKRCWICICVWMAAILSLIPDLVFI	176		
DB 138	MSFESGMLLCLISRYVAIVQSVASHRHRRARVLLISKSCGVIMTAAVLSIPELYS	197		
QY 177	TVNDA-----RCIPRPYRLGTSMKALIMLEICIGFVNPFLIMGVCYRTARTLMKP	231		
DB 198	DLOSSSEQARCLLIENH---VEAFITTIQVQWVIFLVPFLAMSGCYLVIIITLLQAR	254		
QY 232	NKTSRPLKVLNVIVIVITQLPYNTVTKRCRAIDITYSLSLSCSNKSRMDIAIQVYESI	291		
DB 255	NFEHNRKAKIVIAVVVVFVQFLPYNGVLAQVAVNENITSPICELSKQINAVDTYSL	314		
QY 292	ALFHSCLNPLIYVMGASFKNYAKVAKKG-----SW-----RROROSVEEPPD	337		
DB 315	ACVRCVNPFLYAFIAGVFKRNDLFKFLKDLGLCSQDLROMWSCRHIRSSMSVE-----	369		
QY 338	SEGEPTSTPS 349			
DB 370	----AETTTFS 377			

RESULT 4	CKR7_MOUSE	STANDARD;	PRT; 378 AA.
AC	P47774;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	C-C Chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (CCR-7)		
DE	(MIP-3 beta receptor) (BBV-induced G protein-coupled receptor 1) (EBI1).		
DE	CCOR7 OR CCKR7 OR EBI1 OR EBI1H.		
GN	Mus musculus (Mouse).		

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OM protein - protein search, using sw model

Run on: August 6, 2002, 17:57:40 ; Search time 32.78 Seconds
(without alignments)
1185.962 Million cell updates/sec

Title: US-09-686-020a-2

Perfect score: 1819
Sequence: 1 MALRQNSTDYEEENEMNG.....VEPPFDESGTPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: A_Geneseq_032802.*
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23: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	20	AAV57290
2	1819	100.0	350	20	AAV17435
3	1819	100.0	350	20	AAW93169
4	1819	100.0	350	21	AAV94325
5	1819	100.0	350	22	AAAG80119
6	1819	100.0	350	22	AAU08994
7	1819	100.0	350	22	AAAG7237
8	1819	100.0	382	22	AAAG52389
9	1814	99.7	349	20	AAW93170
10	1814	99.7	350	20	AAV30125
11	1810	99.5	350	21	AAV71301

12	1810	99.5	350	21	AAAB02835
13	1808	99.4	350	21	AAAB37788
14	1728	95.0	333	20	AAV57289
15	1620	89.1	350	22	AAAG57238
16	1591	87.5	350	20	AAV57291
17	1275	70.1	246	20	AAV57292
18	1257	69.1	242	22	AAW99494
19	1212	66.6	263	20	AAV30126
20	862	47.4	164	22	ABB11162
21	862	47.4	164	22	AAW79310
22	824	45.3	159	21	AAAB41786
23	761	41.8	175	22	AAW99976
24	761	41.8	175	22	ABBI0276
25	761	41.8	175	22	AAU18115
26	761	41.8	175	22	AAU18361
27	761	41.8	175	22	AAU18669
28	761	41.8	175	22	AAU21655
29	659	36.2	358	15	AAAB3745
30	659	36.2	358	21	AAAB21689
31	659	36.2	378	19	AAW48724
32	659	36.2	378	22	AAAB21688
33	659	36.2	378	22	AAAG80114
34	659	36.2	378	22	AAAB50859
35	659	36.2	410	15	AAAB53743
36	659	36.2	410	19	AAW48723
37	659	36.2	410	21	AAAB21687
38	659	36.2	569	22	ABG12373
39	656	36.1	378	15	AAAB5744
40	655	36.0	378	21	AAV90663
41	653	35.9	378	21	AAV90629
42	650	35.7	378	21	AAAB21699
43	643	35.3	369	22	AAAG80116
44	643	35.3	378	15	AAAB54079
45	643	35.3	378	19	AAW56164

ALIGNMENTS

RESULT 1
AAV57290 standard; Protein; 350 AA.
XX AAV57290;
AC AAV57290;
XX 05-JUN-2000 (first entry)
XX Human BCGK protein.
DE Human BCGK protein.
XX BCGK protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.
XX Homo sapiens.
OS Homo sapiens.
XX WO952945-A2.
PN WO952945-A2.
XX 21-OCT-1999.
PD 21-OCT-1999.
XX 16-APR-1999; 99WO-US08395.
PF 16-APR-1999; 99WO-US08395.
XX 16-APR-1998; 98US-0061753.
PR 16-APR-1999; 99US-0061753.
XX (MILL-) MILLENIUM PHARM INC.
XX Gonzalo JA, Gutierrez-Ramos JC;
XX WPI: 1999-620375/53.
XX N-PSDB; AA290528.
XX New nucleic acid encoding human BCGK receptor, used e.g. for
XX modulating inflammation and tumor growth

XX Claim 8; Fig 2A-B; 123pp; English.
 PS
 XX
 CC The invention relates to a human BGCR protein, a G-protein coupled
 CC receptor. The BGCR protein can be expressed by standard recombinant
 CC methodology. BGCR are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCR nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemottractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the full-length human BGCR protein.
 XX
 XX Sequence 350 AA;
 SQ

Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALEQNSTDYEEENENGTGYSOYELICIKEDVREFAKVLPVFLTIYVIGLAGNS 60
 DB 1 maleqngstdyyeenemngtydygyelickedvrefakvlpvfltiyviglagns 60
 QY 61 MVAATAYAKKQRTKTDVYILNLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSALYT 120
 DB 61 mvaaayaykkqrktldvylnlavaddllftlpfmaavnahgvnlgkimckitsalylt 120
 QY 121 LNFVSMQFLACISIDRYAVATKVPSSGSGVGPWCWMAAILISPOLVFTYVND 180
 DB 121 lnfvsqmgflacisidryavatkvpssgsgvypcwailicvmaaaailispqlvftvnd 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMPNIRKISPLK 240
 DB 181 narcpiprpylgtsmkallqmlaicigfvvpflmgvcyftartlmpnirkisplk 240
 QY 241 VLLTVVIYIVTQLPYNIVKFCRAIDITYSLTSCNMSKRDIAIQVETSIALFHSCINP 300
 DB 241 vlltvviyivtqlpynivkfcraiditysltscnmskrdiaiqvetisialfhscinp 300
 QY 301 ILYVFGASFKNYVMKAKKYSWRROSYEPEPDESGPTSTPSI 350
 DB 301 illyvfmgasfknyvmkakkyswrrqsyveepfdepgptstpsl 350

RESULT 2

AAV17435
 ID AAV17435 standard; Protein; 350 AA.

XX AAV17435;
 XX 29-JUL-1999 (first entry)
 DE Human signal peptide-containing protein SP-16.
 XX
 KW Human; signal peptide-containing protein; SP; cell proliferation;
 KW cancer; neuronal disorder; immune response; detection.
 XX
 OS Homo sapiens.
 XX
 PN W09924463-A2.
 XX
 PD 20-MAY-1999.
 XX
 PF 04-NOV-1998; 98WO-US23578.
 XX
 PR 07-NOV-1997; 97US-0966316.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX

PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
 XX
 XX WPI: 1999-337694/28.
 DR N-PSDB; AAX61288.
 XX
 PT CDNA clones encoding signal peptide-containing proteins
 PS
 XX Claim 1; Fig 1; 83pp; English.
 XX
 CC The present sequence represents a human signal peptide-containing
 CC protein (SP), designated SP-16. SP proteins can be used to stimulate
 CC cell proliferation or to treat or prevent cancer. SP antagonists are
 CC also used to treat or prevent cancer, and also for treating or
 CC preventing neuronal disorders or immune responses. Polynucleotide
 CC sequences complementary to the SP-encoding polynucleotides are useful
 CC for the detection of SP-encoding nucleic acid molecules in biological
 CC samples.
 XX
 XX Sequence 350 AA;
 SQ

Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALEQNSTDYEEENENGTGYSOYELICIKEDVREFAKVLPVFLTIYVIGLAGNS 60
 DB 1 maleqngstdyyeenemngtydygyelickedvrefakvlpvfltiyviglagns 60
 QY 61 MVAATAYAKKQRTKTDVYILNLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSALYT 120
 DB 61 mvaaayaykkqrktldvylnlavaddllftlpfmaavnahgvnlgkimckitsalylt 120
 QY 121 LNFVSMQFLACISIDRYAVATKVPSSGSGVGPWCWMAAILISPOLVFTYVND 180
 DB 121 lnfvsqmgflacisidryavatkvpssgsgvypcwailicvmaaaailispqlvftvnd 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMPNIRKISPLK 240
 DB 181 narcpiprpylgtsmkallqmlaicigfvvpflmgvcyftartlmpnirkisplk 240
 QY 241 VLLTVVIYIVTQLPYNIVKFCRAIDITYSLTSCNMSKRDIAIQVETSIALFHSCINP 300
 DB 241 vlltvviyivtqlpynivkfcraiditysltscnmskrdiaiqvetisialfhscinp 300
 QY 301 ILYVFGASFKNYVMKAKKYSWRROSYEPEPDESGPTSTPSI 350
 DB 301 illyvfmgasfknyvmkakkyswrrqsyveepfdepgptstpsl 350

RESULT 3

AAW93169
 ID AAW93169 standard; Protein; 350 AA.

XX AAW93169;
 XX 24-MAY-1999 (first entry)
 DE Human HFINO41 protein.
 XX
 KW HFINO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
 KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
 KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
 KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
 KW benign prostatic hypertrophy; psychologic disorder; neurological disorder;
 KW anxiety; manic depression; delirium; dementia; severe mental retardation;
 KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW linkage analysis; gene mapping; human.
 XX
 OS Homo sapiens.
 XX

PN EP899332-A2.
 PD 03-MAR-1999.
 XX
 PF 17-FEB-1998; 98BP-0301170.
 XX
 PR 27-OCT-1997; 97US-0962922.
 PR 15-AUG-1997; 97US-0055895.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI ELLIS CE;
 DR WPI; 1999-144803/13.
 DR N-PSDB; AAX22557.
 XX
 PT New G-coupled receptor (HTR041) polypeptide and polynucleotide -
 PT useful as diagnostic reagents and for prevention and treatment of
 PT cancer, HIV infections and Parkinson's disease
 XX
 PS Claim 1; Page 22-23; 27pp; English.
 XX
 CC This sequence represents a G-coupled receptor, HTR041 which is useful
 CC for diagnosing susceptibility to diseases by detecting mutations in the
 CC HTR041 gene, and can diagnose diseases associated with HTR041 protein
 CC imbalance by determining HTR041 polypeptide expression levels. Agonists
 CC and antagonists of the protein can be used in treatment to activate
 CC (agonist) or inhibit (antagonist) HTR041 activity, in addition to direct
 CC administration of antisense sequences to prevent expression, or HTR041
 CC polynucleotides to treat conditions associated with a lack of HTR041
 CC protein. Gene therapy may also be used to affect endogenous HTR041
 CC polypeptide expression. HTR041 antibodies are useful for inducing an
 CC immune response to immunize and prevent disease, and for isolating
 CC HTR041 clones or purifying the polypeptides by affinity chromatography.
 CC HTR041 polypeptides can be administered directly or as a vaccine to
 CC inoculate against disease. Diseases diagnosed, prevented and treated
 CC include bacterial, fungal, protozoan and viral infections, particularly
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
 CC disease; acute heart failure; hypotension; hypertension; urinary
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
 CC asthma; allergies; benign prostatic hypertrophy; and psychotropic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, delirium, dementia, severe mental retardation and dyskinesias
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
 CC HTR041 polypeptide is also useful for mapping the gene to a chromosome,
 CC allowing gene inheritance to be studied through linkage analysis.
 XX
 XX Sequence 350 AA:
 SQ
 Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 ILVFMGASFKNYVMYAKKYGSMRROGSEEPFDSGPTPTSTFST 350
 DB 301 ILVFMGASFKNYVMYAKKYGSMRROGSEEPFDSGPTPTSTFST 350
 RESULT 4
 ID AAY94325
 AAY94325 standard; Protein; 350 AA.
 XX
 AC AAY94325;
 XX
 AC AAY94325;
 XX
 DT 11-AUG-2000 (first entry)
 XX
 DE Human seven transmembrane receptor VSHK-1.
 XX
 KW Human; seven transmembrane receptor; VSHK-1; signal transduction.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6..8
 FT Modified-site /note= "potential N-glycosylation site"
 FT Modified-site /note= "potential N-glycosylation site"
 FT Domain 42..66
 FT Domain /label= Transmembrane_domain
 FT Domain 79..100
 FT Domain /label= Transmembrane_domain
 FT Domain 114..135
 FT Domain /label= Transmembrane_domain
 FT Domain 156..175
 FT Domain /label= Transmembrane_domain
 FT Domain 199..221
 FT Domain /label= Transmembrane_domain
 FT Domain 241..262
 FT Domain /label= Transmembrane_domain
 FT Modified-site 276..278
 FT Modified-site /note= "potential N-glycosylation site"
 FT Domain 287..308
 FT Domain /label= Transmembrane_domain
 XX
 XX W0200026369-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US25848.
 XX
 PR 04-NOV-1998; 98US-0107112.
 PR 06-JUN-1999; 99US-0114856.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 PI Khoja H, Shymala V;
 DR WPI; 2000-365618/31.
 DR N-PSDB; AAY94325.
 XX
 PT Novel polypeptide comprising a new seven-transmembrane receptor protein
 PT and its encoding polynucleotide, useful for the analysis of VSHK-1.
 XX
 PS Claim 3; Fig 1; 79pp; English.
 XX
 CC The present sequence is VSHK-1, a new seven transmembrane
 CC receptor which contains seven membrane-spanning helical domains
 CC that are linked by three intracellular and three extracellular loops. The
 CC gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart
 CC tissue, where VSHK-1 is predominantly found, three RNA species were
 CC identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide
 CC encoding the present sequence corresponds to the 2.0kb form. The 1.3kb
 CC form may result from the use of an alternative polyadenylation site while
 CC transcription of a 3.0kb intron at nucleotide 74 could account for the
 CC 5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes

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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:04:30 : Search time 13.09 Seconds
(Without alignments) 653.091 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONQSDIYYEENEMNG.....VEEPDSDGTEPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTCDS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16
2	1620	89.1	350	2	US-08-966-316-18
3	659	36.2	358	1	US-08-153-848-19
4	659	36.2	358	4	US-09-299-843A-19
5	659	36.2	358	4	US-09-088-337B-19
6	659	36.2	358	5	PCT-US93-11153-19
7	659	36.2	378	1	US-08-153-848-15
8	659	36.2	378	3	US-09-299-843A-15
9	659	36.2	378	4	US-09-251-545-1
10	659	36.2	378	4	US-09-088-337B-15
11	659	36.2	378	5	PCT-US93-11153-15
12	659	36.2	410	1	US-08-153-848-7
13	659	36.2	410	3	US-09-299-843A-7
14	659	36.2	410	3	US-09-088-337B-7
15	659	36.2	410	5	PCT-US93-11153-7
16	650	35.7	378	3	US-09-299-843A-66
17	650	35.7	378	4	US-09-088-337B-66
18	643	35.3	378	1	US-08-383-750-2
19	643	35.3	378	1	US-08-383-751A-2
20	643	35.3	378	3	US-08-352-678-2
21	643	35.3	378	4	US-09-045-583-49
22	643	35.3	378	5	PCT-US93-09636-2
23	637	35.0	357	4	US-09-266-464-2
24	635.5	34.9	359	1	US-08-153-848-24
25	635.5	34.9	359	1	US-09-299-843A-24
26	635.5	34.9	359	4	US-09-088-337B-24
27	635.5	34.9	359	5	PCT-US93-11153-24

28	606.5	33.3	361	2	US-08-902-294-2	Sequence 2, Appl1
29	606.5	33.3	361	3	US-09-178-637-2	Sequence 2, Appl1
30	583	32.1	374	4	US-09-045-583-48	Sequence 48, Appl1
31	581	31.9	342	4	US-09-116-498-4	Sequence 4, Appl1
32	569	31.3	342	4	US-09-116-498-6	Sequence 6, Appl1
33	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appl1
34	560	30.8	342	4	US-09-275-384B-5	Sequence 5, Appl1
35	560	30.8	342	4	US-09-116-498-2	Sequence 2, Appl1
36	560	30.8	342	4	US-09-449-437A-2	Sequence 20, Appl1
37	537.5	29.5	360	4	US-08-875-573-20	Sequence 20, Appl1
38	537.5	29.5	360	4	US-09-232-878-2	Sequence 2, Appl1
39	537.5	29.5	360	4	US-09-045-583-55	Sequence 55, Appl1
40	534.5	29.4	355	1	US-07-759-568-1	Sequence 1, Appl1
41	534.5	29.4	355	1	US-08-450-393A-8	Sequence 8, Appl1
42	534.5	29.4	355	2	US-08-390-000A-5	Sequence 8, Appl1
43	534.5	29.4	355	4	US-08-446-669-8	Sequence 8, Appl1
44	534.5	29.4	355	5	PCT-US95-00476-8	Sequence 8, Appl1
45	534.5	29.4	360	1	US-08-202-056-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-966-316-16
Sequence 16, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preetie
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNOT11
CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 7.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MALEONOSTDYEEENEMNGTIDYDSEYELICIKEDVREFAKVELPVELTIVFVIGLANS 60
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1 MALEONOSTDYEEENEMNGTIDYDSEYELICIKEDVREFAKVELPVELTIVFVIGLANS 60
61 MVAIAVYKRTKRTDYIILNLAVALDLFLFTLPFAVNAVHGVGLKIMCKITSALYT 120
61 MVAIAVYKRTKRTDYIILNLAVALDLFLFTLPFAVNAVHGVGLKIMCKITSALYT 120
121 LNFVSGMOFLACISIDRYAVATKVPDSQGVKPCWICFCVMAAILLISIPOLVFTVND 180
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181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIRKISRLK 240
181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIRKISRLK 240
241 VLTAVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRMIDIAIOVTEISALFHSCLNP 300
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301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDSGPTSTESI 350
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RESULT 2

US-08-966-316-18
Sequence 18, Application US/08966316
Patent No. 5932445

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Koopa
APPLICANT: Murry, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 399711
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 7.1e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

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1 MALEONOSTDYEEENEMNGTIDYDSEYELICIKEDVREFAKVELPVELTIVFVIGLANS 60
1 MALEONOSTDYEEENEMNGTIDYDSEYELICIKEDVREFAKVELPVELTIVFVIGLANS 60
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241 VLTAVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRMIDIAIOVTEISALFHSCLNP 300
301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDSGPTSTESI 350
301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDSGPTSTESI 350

RESULT 3

US-08-153-848-19
Sequence 19, Application US/08153848
Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300